

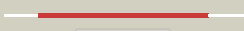






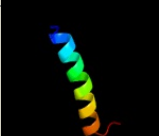





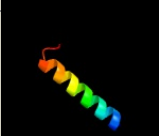



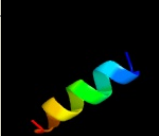







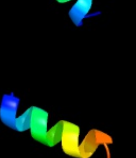


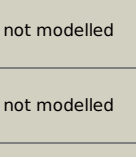


Phyre2

| | |
|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3259_(-)_3639422_3639841 |
| Date | Thu Aug 8 16:20:46 BST 2019 |
| Unique Job ID | 2c01aed07e39d138 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | d3e11a1 |  Alignment |  | 100.0 | 20 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TTHA0227-like |
| 2 | d2ejqa1 |  Alignment |  | 99.9 | 12 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TTHA0227-like |
| 3 | c2j83B_ |  Alignment |  | 94.3 | 8 | PDB header: hydrolase Chain: B: PDB Molecule: ulilysin; PDBTitle: ulilysin metalloprotease in complex with batimastat. |
| 4 | d1k7ia2 |  Alignment |  | 93.6 | 11 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain |
| 5 | c3lmcA_ |  Alignment |  | 92.4 | 8 | PDB header: hydrolase Chain: A: PDB Molecule: peptidase, zinc-dependent; PDBTitle: crystal structure of zinc-dependent peptidase from methanocorpusculum2 labreanum (strain z), northeast structural genomics consortium target3 mur16 |
| 6 | c2xhqA_ |  Alignment |  | 92.2 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: archaemetzincin; PDBTitle: crystal structure of archaemetzincin (amza) from archaeoglobus2 fulgidus at 1.45 a resolution |
| 7 | d1y93a1 |  Alignment |  | 91.4 | 19 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain |
| 8 | c2x7mA_ |  Alignment |  | 91.4 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: archaemetzincin; PDBTitle: crystal structure of archaemetzincin (amza) from methanopyrus2 kandleri at 1.5 a resolution |
| 9 | d1rm8a_ |  Alignment |  | 91.3 | 19 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain |
| 10 | d1qiba_ |  Alignment |  | 91.2 | 6 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain |
| 11 | d1hv5a_ |  Alignment |  | 91.2 | 13 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain |

| | | | | | | |
|----|-------------------------|-----------|---|------|----|---|
| 12 | d2ovxa1 | Alignment |  | 91.2 | 25 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain |
| 13 | d1bqqm_ | Alignment |  | 91.1 | 13 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain |
| 14 | c2xs4A_ | Alignment |  | 91.0 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: karilysin protease; PDBTitle: structure of karilysin catalytic mmp domain in complex with magnesium |
| 15 | d1cgla_ | Alignment |  | 90.5 | 19 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain |
| 16 | d1mmqa_ | Alignment |  | 90.4 | 6 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain |
| 17 | d1hova_ | Alignment |  | 90.3 | 6 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain |
| 18 | d1eaka2 | Alignment |  | 90.2 | 13 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain |
| 19 | d1q3aa_ | Alignment |  | 89.9 | 13 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain |
| 20 | d1hy7a_ | Alignment |  | 89.9 | 13 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain |
| 21 | d1i76a_ | Alignment | not modelled | 89.9 | 13 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain |
| 22 | d1hfca_ | Alignment | not modelled | 89.6 | 19 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain |
| 23 | d1xuca1 | Alignment | not modelled | 89.3 | 19 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain |
| 24 | c2jsdA_ | Alignment | not modelled | 89.2 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: matrix metalloproteinase-20; PDBTitle: solution structure of mmp20 complexed with nngH |
| 25 | d1sata2 | Alignment | not modelled | 89.0 | 7 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain |
| 26 | d1g9ka2 | Alignment | not modelled | 88.9 | 13 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain |
| 27 | d1kapp2 | Alignment | not modelled | 88.8 | 13 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain |
| 28 | d1cxva_ | Alignment | not modelled | 88.6 | 13 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain |
| 29 | c1clmA | Alignment | not modelled | 88.5 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: stromelysin-1; |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c1sima_ | Alignment | not modelled | 88.3 | 13 | PDBTitle: crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme PDB header: hydrolase |
| 30 | c2mzeA_ | Alignment | not modelled | 88.3 | 6 | Chain: A: PDB Molecule: matrilysin; PDBTitle: nmr solution structure of the pro form of human matrilysin (prommp-7) |
| 31 | c5th6D_ | Alignment | not modelled | 87.5 | 19 | PDB header: hydrolase/hydrolase inhibitor Chain: D: PDB Molecule: matrix metalloproteinase-9,matrix metalloproteinase-9; PDBTitle: structure determination of a potent, selective antibody inhibitor of2 human mmp9 (apo mmp9) |
| 32 | d1fbla2 | Alignment | not modelled | 87.1 | 13 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain |
| 33 | c1su3A_ | Alignment | not modelled | 86.6 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: interstitial collagenase; PDBTitle: x-ray structure of human prommp-1: new insights into2 collagenase action |
| 34 | c4g0dD_ | Alignment | not modelled | 86.2 | 19 | PDB header: hydrolase Chain: D: PDB Molecule: collagenase 3; PDBTitle: human collagenase 3 (mmp-13) full form with peptides from pro-domain |
| 35 | c2cltB_ | Alignment | not modelled | 86.1 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: interstitial collagenase; PDBTitle: crystal structure of the active form (full-length) of human2 fibroblast collagenase. |
| 36 | c1jiwP_ | Alignment | not modelled | 84.8 | 13 | PDB header: hydrolase/hydrolase inhibitor Chain: P: PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex |
| 37 | c5czwA_ | Alignment | not modelled | 84.5 | 7 | PDB header: hydrolase Chain: A: PDB Molecule: myroilysin; PDBTitle: crystal structure of myroilysin |
| 38 | c3ba0A_ | Alignment | not modelled | 84.4 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: macrophage metalloelastase; PDBTitle: crystal structure of full-length human mmp-12 |
| 39 | c1om8A_ | Alignment | not modelled | 83.8 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: serralysin; PDBTitle: crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallized with 10 mm edta |
| 40 | c3b8zB_ | Alignment | not modelled | 80.4 | 7 | PDB header: hydrolase Chain: B: PDB Molecule: protein adams-5; PDBTitle: high resolution crystal structure of the catalytic domain of adams-52 (aggrecanase-2) |
| 41 | d1atla_ | Alignment | not modelled | 77.7 | 6 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like |
| 42 | c3k7IA_ | Alignment | not modelled | 76.3 | 6 | PDB header: hydrolase Chain: A: PDB Molecule: atragin; PDBTitle: structures of two elapid snake venom metalloproteases with2 distinct activities highlight the disulfide patterns in the3 d domain of adamalysin family proteins |
| 43 | d1kufa_ | Alignment | not modelled | 76.1 | 7 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like |
| 44 | d4aiga_ | Alignment | not modelled | 75.7 | 6 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like |
| 45 | c3lqbA_ | Alignment | not modelled | 75.6 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: loc792177 protein; PDBTitle: crystal structure of the hatching enzyme zhe1 from the zebrafish danio2 rerio |
| 46 | c3vtgA_ | Alignment | not modelled | 75.5 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: high choriolytic enzyme 1; PDBTitle: high choriolytic enzyme 1 (hce-1), a hatching enzyme zinc-protease2 from oryzias latipes (medaka fish) |
| 47 | c2i47A_ | Alignment | not modelled | 75.2 | 0 | PDB header: hydrolase Chain: A: PDB Molecule: adam 17; PDBTitle: crystal structure of catalytic domain of tace with inhibitor |
| 48 | d1asta_ | Alignment | not modelled | 75.1 | 8 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Astacin |
| 49 | d2i47a1 | Alignment | not modelled | 75.1 | 0 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TNF-alpha converting enzyme, TACE, catalytic domain |
| 50 | d1nd1a_ | Alignment | not modelled | 75.0 | 12 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like |
| 51 | c4dd8B_ | Alignment | not modelled | 74.8 | 13 | PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: disintegrin and metalloproteinase domain-containing protein PDBTitle: adam-8 metalloproteinase domain with bound batimastat |
| 52 | d1quaa_ | Alignment | not modelled | 74.1 | 7 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like |
| 53 | d1r55a_ | Alignment | not modelled | 73.9 | 7 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like |
| 54 | c3edhA_ | Alignment | not modelled | 73.6 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: bone morphogenetic protein 1; PDBTitle: crystal structure of bone morphogenetic protein 1 protease2 domain in complex with partially bound dmso |
| 55 | c1yp1A_ | Alignment | not modelled | 73.5 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: fii; PDBTitle: crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | metalloproteinase from venom of agkistrodon acutus PDB header: hydrolase Chain: A: PDB Molecule: immune inhibitor a, metalloprotease; PDBTitle: crystal structure of selenomethionine variant of bacillus anthracis2 immune inhibitor a2 peptidase zymogen |
| 56 | c4yu5A_ | Alignment | not modelled | 73.4 | 7 | PDB header: hydrolase, blood clotting, toxin Chain: A: PDB Molecule: coagulation factor x-activating enzyme heavy chain; PDBTitle: crystal structure of russell's viper venom metalloproteinase |
| 57 | c2e3xA_ | Alignment | not modelled | 72.9 | 12 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like |
| 58 | d1wnia_ | Alignment | not modelled | 72.7 | 7 | PDB header: hydrolase Chain: A: PDB Molecule: adamts-5; PDBTitle: crystal structure of adamts5 with inhibitor bound |
| 59 | c2rjqA_ | Alignment | not modelled | 72.4 | 7 | PDB header: apoptosis, toxin Chain: B: PDB Molecule: catrocollastatin; PDBTitle: crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal) |
| 60 | c2dw1B_ | Alignment | not modelled | 72.2 | 12 | PDB header: membrane protein Chain: D: PDB Molecule: disintegrin and metalloproteinase domain-containing protein PDBTitle: adam10 extracellular domain |
| 61 | c6be6D_ | Alignment | not modelled | 71.9 | 12 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Zinc protease |
| 62 | d1c7ka_ | Alignment | not modelled | 71.8 | 7 | PDB header: toxin Chain: A: PDB Molecule: vascular apoptosis-inducing protein 1; PDBTitle: crystal structure of vascular apoptosis-inducing protein-1 (inhibitor-2 bound form) |
| 63 | c2erpA_ | Alignment | not modelled | 71.5 | 18 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like |
| 64 | d1bswa_ | Alignment | not modelled | 70.9 | 29 | PDB header: membrane protein Chain: A: PDB Molecule: adam 22; PDBTitle: structural and biochemical studies on the ectodomain of human adam22 |
| 65 | c3g5cA_ | Alignment | not modelled | 70.3 | 18 | PDB header: hydrolase Chain: C: PDB Molecule: adamts-4; PDBTitle: crystal structure of adamts4 with inhibitor bound |
| 66 | c2rjpC_ | Alignment | not modelled | 70.2 | 6 | PDB header: hydrolase Chain: B: PDB Molecule: adamts-1; PDBTitle: crystal structure of human adamts-1 catalytic domain and cysteine-2 rich domain (apo-form) |
| 67 | c2v4bB_ | Alignment | not modelled | 69.8 | 0 | PDB header: hydrolase Chain: A: PDB Molecule: k-like; PDBTitle: structures of two elapid snake venom metalloproteases with2 distinct activities highlight the disulfide patterns in the3 d domain of adamalysin family proteins |
| 68 | c3k7nA_ | Alignment | not modelled | 68.2 | 12 | PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: 72 kda type iv collagenase; PDBTitle: catalytic domain of prommp-2 e404q mutant |
| 69 | c1eakA_ | Alignment | not modelled | 64.6 | 7 | PDB header: hydrolase Chain: B: PDB Molecule: projanalysin; PDBTitle: crystal structure of the metallopeptidase zymogen of2 methanocaldococcus jannaschii jannalysin |
| 70 | c4jixB_ | Alignment | not modelled | 63.9 | 33 | PDB header: hydrolase Chain: A: PDB Molecule: proastacin; PDBTitle: zymogen structure of crayfish astacin metallopeptidase |
| 71 | c3lq0A_ | Alignment | not modelled | 61.0 | 8 | PDB header: hydrolase Chain: B: PDB Molecule: probable protease htpx homolog; PDBTitle: crystal structure of heat shock protein htpx domain from vibrio2 parahaemolyticus rimd 2210633 |
| 72 | c3cqbb_ | Alignment | not modelled | 59.7 | 15 | PDB header: hydrolase Chain: B: PDB Molecule: metallo-endopeptidase; PDBTitle: crystal structure of a metallo-endopeptidases (bacova_00663) from2 bacteroides ovatus at 1.93 a resolution |
| 73 | c3p1vB_ | Alignment | not modelled | 59.5 | 6 | PDB header: hydrolase Chain: A: PDB Molecule: ecxa; PDBTitle: gm1 bound form of the ecx ab5 holotoxin |
| 74 | c4l6tA_ | Alignment | not modelled | 59.1 | 17 | PDB header: hydrolase Chain: B: PDB Molecule: caax prenyl protease 1 homolog; PDBTitle: crystal structure of the human nuclear membrane zinc metalloprotease2 zmpste24 (face1) |
| 75 | c4aw6B_ | Alignment | not modelled | 57.6 | 29 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Leishmanalysin |
| 76 | d1lmla_ | Alignment | not modelled | 57.5 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: proabylysin; PDBTitle: crystal structure of the metallopeptidase zymogen of pyrococcus abyssi2 abylysin |
| 77 | c4jiuA_ | Alignment | not modelled | 52.2 | 25 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative zinc-binding metallo-peptidase2 (baccac_01431) from bacteroides caccae atcc 43185 at 2.10 a3 resolution |
| 78 | c4l7aB_ | Alignment | not modelled | 51.1 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: meprin a subunit beta; PDBTitle: crystal structure of human mature meprin beta |
| 79 | c4gwnA_ | Alignment | not modelled | 50.6 | 13 | PDB header: transport protein Chain: A: PDB Molecule: polyketide synthase pks13; PDBTitle: 1.16 angstrom resolution crystal structure of acyl carrier protein2 domain (residues 1-100) of polyketide synthase pks13 from3 mycobacterium tuberculosis |
| 80 | c6c4qA_ | Alignment | not modelled | 50.6 | 19 | Fold: IF3-like |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|--|
| 81 | d1whra_ | Alignment | not modelled | 47.9 | 40 | Superfamily: R3H domain Family: R3H domain |
| 82 | c2n98A_ | Alignment | not modelled | 47.4 | 31 | PDB header: transport protein Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: solution structure of acyl carrier protein lipid from actinoplanes2 friuliensis |
| 83 | c3mlcC_ | Alignment | not modelled | 45.3 | 15 | PDB header: isomerase Chain: C: PDB Molecule: fg41 malonate semialdehyde decarboxylase; PDBTitle: crystal structure of fg41msad inactivated by 3-chloropropiolate |
| 84 | c4gwmA_ | Alignment | not modelled | 45.0 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: meprin a subunit beta; PDBTitle: crystal structure of human promeprin beta |
| 85 | c3p24C_ | Alignment | not modelled | 44.6 | 9 | PDB header: hydrolase Chain: C: PDB Molecule: bft-3; PDBTitle: structure of profragilysin-3 from bacteroides fragilis |
| 86 | c5xbvA_ | Alignment | not modelled | 44.4 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: wss1p; PDBTitle: crystal structure of wss1 mutant from saccharomyces cerevisiae |
| 87 | c3ujzA_ | Alignment | not modelled | 43.6 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: metalloprotease stce; PDBTitle: crystal structure of enterohemorrhagic e. coli stce |
| 88 | c5un4C_ | Alignment | not modelled | 43.1 | 16 | PDB header: hydrolase Chain: C: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of native fused 4-ot |
| 89 | c4on1B_ | Alignment | not modelled | 41.6 | 18 | PDB header: hydrolase Chain: B: PDB Molecule: putative metalloprotease ii; PDBTitle: crystal structure of metalloproteinase-ii from bacteroides fragilis |
| 90 | c6o38A_ | Alignment | not modelled | 39.9 | 17 | PDB header: sugar binding protein Chain: A: PDB Molecule: acinetobacter secreted protease cpaa; PDBTitle: structure of a chaperone-substrate complex |
| 91 | c5ln5A_ | Alignment | not modelled | 38.7 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin and wlm domain-containing metalloprotease PDBTitle: crystal structure of the wss1 e203q mutant from s. pombe |
| 92 | d1z67a1 | Alignment | not modelled | 38.4 | 29 | Fold: YidB-like Superfamily: YidB-like Family: YidB-like |
| 93 | c4ca3A_ | Alignment | not modelled | 37.9 | 24 | PDB header: ribosomal protein Chain: A: PDB Molecule: hybrid polyketide synthase-non ribosomal peptide PDBTitle: solution structure of streptomyces virginiae vira acp5b |
| 94 | c6eomA_ | Alignment | not modelled | 37.3 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: structure of dpp iii from caldithrix abyssi |
| 95 | c2op8A_ | Alignment | not modelled | 35.8 | 13 | PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase ywhb; PDBTitle: crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase |
| 96 | c1z5hB_ | Alignment | not modelled | 35.5 | 12 | PDB header: hydrolase Chain: B: PDB Molecule: tricorn protease interacting factor f3; PDBTitle: crystal structures of the tricorn interacting factor f3 from2 thermoplasma acidophilum |
| 97 | c3ry0A_ | Alignment | not modelled | 34.9 | 18 | PDB header: isomerase Chain: A: PDB Molecule: putative tautomerase; PDBTitle: crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway |
| 98 | d2aala1 | Alignment | not modelled | 34.7 | 14 | Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MSAD-like |
| 99 | c2x4kB_ | Alignment | not modelled | 34.0 | 11 | PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa) |
| 100 | c1l6jA_ | Alignment | not modelled | 33.6 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: matrix metalloproteinase-9; PDBTitle: crystal structure of human matrix metalloproteinase mmp92 (gelatinase b). |
| 101 | c1satA_ | Alignment | not modelled | 33.0 | 7 | PDB header: hydrolase (serine protease) Chain: A: PDB Molecule: serratia protease; PDBTitle: crystal structure of the 50 kda metallo protease from s.2 marcescens |
| 102 | d1j7na2 | Alignment | not modelled | 31.4 | 8 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Anthrax toxin lethal factor, N- and C-terminal domains |
| 103 | c3mb2G_ | Alignment | not modelled | 31.3 | 11 | PDB header: isomerase Chain: G: PDB Molecule: 4-oxalocrotonate tautomerase family enzyme - alpha subunit; PDBTitle: kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily |
| 104 | d1xm5a_ | Alignment | not modelled | 31.2 | 20 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Predicted metal-dependent hydrolase |
| 105 | c1gxdA_ | Alignment | not modelled | 30.0 | 0 | PDB header: hydrolase Chain: A: PDB Molecule: 72 kda type iv collagenase; PDBTitle: prommp-2/timp-2 complex |
| | | | | | | PDB header: hydrolase |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|--|
| 106 | c4il3B_ | Alignment | not modelled | 30.0 | 25 | Chain: B: PDB Molecule: ste24p; PDBTitle: crystal structure of s. mikatae ste24p |
| 107 | c2afdA_ | Alignment | not modelled | 29.6 | 42 | PDB header: ligand binding protein Chain: A: PDB Molecule: protein asl1650; PDBTitle: solution structure of asl1650, an acyl carrier protein from anabaena2 sp. pcc 7120 with a variant phosphopantetheinylation-site sequence |
| 108 | d1l8qa1 | Alignment | not modelled | 27.1 | 33 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Chromosomal replication initiation factor DnaA C-terminal domain IV |
| 109 | d1tvia_ | Alignment | not modelled | 26.1 | 15 | Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Predicted metal-dependent hydrolase |
| 110 | c1l0oC_ | Alignment | not modelled | 25.6 | 27 | PDB header: protein binding Chain: C: PDB Molecule: sigma factor; PDBTitle: crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf |
| 111 | d1l0oc_ | Alignment | not modelled | 25.6 | 27 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain |
| 112 | d1msza_ | Alignment | not modelled | 24.9 | 27 | Fold: IF3-like Superfamily: R3H domain Family: R3H domain |
| 113 | c1mszA_ | Alignment | not modelled | 24.9 | 27 | PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein smubp-2; PDBTitle: solution structure of the r3h domain from human smubp-2 |
| 114 | c5zumB_ | Alignment | not modelled | 24.6 | 25 | PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl-peptidase iii; PDBTitle: structure of dipeptidyl-peptidase iii from coralloccoccus sp. strain2 egb |
| 115 | c2ju2A_ | Alignment | not modelled | 24.5 | 19 | PDB header: transferase Chain: A: PDB Molecule: erythronolide synthase; PDBTitle: minimized mean solution structure of the acyl carrier2 protein domain from module 2 of 6-deoxyerythronolide b3 synthase (debs) |
| 116 | c2mf4A_ | Alignment | not modelled | 24.2 | 23 | PDB header: transferase Chain: A: PDB Molecule: hybrid polyketide synthase-non ribosomal peptide PDBTitle: 1h, 13c, 15n chemical shift assignments of streptomyces virginiae vira2 acp5a |
| 117 | c3dl1A_ | Alignment | not modelled | 23.7 | 40 | PDB header: hydrolase Chain: A: PDB Molecule: putative metal-dependent hydrolase; PDBTitle: crystal structure of a putative metal-dependent hydrolase2 (yp_001336084.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 2.20 a resolution |
| 118 | d2ou3a1 | Alignment | not modelled | 23.7 | 16 | Fold: TerB-like Superfamily: TerB-like Family: COG3793-like |
| 119 | d1otfa_ | Alignment | not modelled | 23.2 | 11 | Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like |
| 120 | c3s8mA_ | Alignment | not modelled | 23.2 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-acp reductase; PDBTitle: the crystal structure of fabv |